RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/005,318C

DATE: 02/06/2001 TIME: 15:57:09

Imput Set : A:\401c1.app

Output Set: N:\CRF3\02062001\I005318C.raw

## SEQUENCE LISTING

```
4 (1) GENERAL INFORMATION:
C--> 6
            (i) APPLICANT: Hein, Mich B.
                           Hiatt, Andrew C.
                           Fitchen, John H.
            (ii) TITLE OF INVENTION: NOVEL EPITHELIAL TISSUE TARGETING AGENT
     10
     12
           (iii) NUMBER OF SEQUENCES: 140
            (iv) CORRESPONDENCE ADDRESS:
     15
                  (A) ADDRESSEE: SEED IP LAW GROUP PLLC
                  (B) STREET: 701 Fifth Avenue, Suite 6300
     16
     17
                  (C) CITY: Seattle
     18
                  (D) STATE: Washington
                  (E) COUNTRY: USA
     20
                  (F) ZIP: 98104
     22
            (V) COMPUTER READABLE FORM:
     23
                  (A) MEDIUM TYPE: Floppy disk
                  (B) COMPUTER: IBM PC compatible
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     26
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
     28
           (vi) CURRENT APPLICATION DATA:
C--> 29
                  (A) APPLICATION NUMBER: US/09/005,318C
C--> 30
                  (B) FILING DATE: 09-Jan-1998
     31
                  (C) CLASSIFICATION:
     33
          (viii) ATTORNEY/AGENT INFORMATION:
                  (A) NAME: Christiansen, William T.
     35
                  (B) REGISTRATION NUMBER: 44,614
                  (C) REFERENCE/DOCKET NUMBER: 310098.401C1
     36
     38
           (ix) TELECOMMUNICATION INFORMATION:
     39
                  (A) TELEPHONE: (206) 622-4900
     40
                  (B) TELEFAX: (206) 682-6031
    43 (2) INFORMATION FOR SEQ ID NO: 1:
     45
            (i) SEQUENCE CHARACTERISTICS:
     46
                  (A) LENGTH: 137 amino acids
     47
                 (B) TYPE: amino acid
                 (C) STRANDEDNESS:
     48
     49
                 (D) TOPOLOGY: linear
     55
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     57
            Gin Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys Cys Ala
     58
            1 5 10
     60
            Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu Asp
     6.1
                       20
            Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg Glu
     64
                    35
                                        40
                                                            45
     66
            Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Pro Val Tyr His
     67
                                   55
     69
            Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu Asp
```

## **ENTERED**

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RAW SEQUENCE LISTING DATE: 02/06/2001 PATENT APPLICATION: US/09/005,318C TIME: 15:57:09

Input Set : A:\401cl.app

Output Set: N:\CRF3\02062001\1005318C.raw

```
72
        Asn Gln Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp Ser
73
                       8.5
                                           90
75
        Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Ala
76
                  100
                                     105
                                                         1.10
78
        Val Val Pro Leu Val Tyr Gly Gly Glu Thr Lys Met Val Glu Thr Ala
79
              115
                                120
                                                       125
        Leu Thr Pro Asp Ala Cys Tyr Pro Asp
81
82
           130
                              135
84 (2)
      INFORMATION FOR SEQ ID NO: 2:
        (i) SEQUENCE CHARACTERISTICS:
86
87
             (A) LENGTH: 135 amino acids
             (B) TYPE: amino acid
89
             (C) STRANDEDNESS:
             (D) TOPOLOGY: linear
90
96
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
        Gln Asp Glu Asn Glu Arg Tle Val Val Asp Asn Lys Cys Lys Cys Ala
98
99
                                          10
        Arg Ile Thr Ser Arg Ile Ile Pro Ser Ala Glu Asp Pro Ser Gin Asp 20 25 30
101
102
104
         Ile Val Glu Arg Asn Val Arg Ile Ile Val Pro Leu Asn Ser Arg Glu
105
               35
                                   40
                                                       4.5
1.07
         Asn Ile Ser Asp Pro Thr Ser Pro Met Arg Thr Lys Pro Val Tyr His
108
                       55
110
         Leu Ser Asp Leu Cys Lys Lys Cys Asp Thr Thr Glu Val Glu Leu Glu
111
                          7.0
                                              7.5
113
         Asp Gln Val Val Thr Ala Ser Gln Ser Asn Ile Cys Asp Ser Asp Ala
114
                      85
                                            90
116
         Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Asn Arg Val
117
                    100
                                       105
                                                          110
119
         Lys Leu Ser Tyr Arg Gly Gln Thr Lys Met Val Glu Thr Ala Leu Thr
120
              115
122
        Pro Asp Ser Cys Tyr Pro Asp
123
           130
                              135
126 (2) INFORMATION FOR SEQ ID NO: 3:
128
         (i) SEQUENCE CHARACTERISTICS:
1.29
             (A) LENGTH: 137 amino acids
130
             (B) TYPE: amino acid
131
             (C) STRANDEDNESS:
132
             (D) TOPOLOGY: linear
138
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
        Asp Asp Glu Ala Thr Ile Leu Ala Asp Asn Lys Cys Met Cys Thr Arg
141
                       5
                                           10
                                                              15
143
        Val Thr Ser Arg Ile Ile Pro Ser Thr Glu Asp Pro Asn Glu Asp Ile
144
              20
                                   25
146
        Val Glu Arg Asn Ile Arg Ile Val Val Pro Leu Asn Asn Arg Glu Asn
              35
                                 40
                                                     4.5
149
        Ile Ser Asp Pro Thr Ser Pro Leu Arg Arg Asn Pro Val Tyr His Leu
150
                               55
152
        Ser Asp Val Cys Lys Lys Cys Asp Pro Val Glu Val Glu Leu Glu Asp
```

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PATENT APPLICATION: US/09/005,318C TIME: 15:57:09

Input Set : A:\401c1.app

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153	65		70					75					80
155	Gln Val	Val Thr	Ala Th	r Gln	Ser	Asn	rle	Cvs	Asn	G I ii	Asn	Δen	00
156			85				90					95	, G.E.y
158	Val Pro	Glu Thr	Cys Ty	r Met	TVE	Asp	Ara	Ası	Lvs	Cve	dvr	· mbr	'llh ~
159		100			••	105	.,		1-		110		1111
161	Met Val	Pro Leu	Arg Ty	r His	Glv		Thr	five	Mot	Val	G10	Ala	Λla
162		11.5			120					125		A1.u	Alu
164	Leu Thr	Pro Asp	Ser Cy	s Tyr	Pro	Asp				.1.4.7			
165	130		•	135		1.							
167 (2)	INFORMATI	ON FOR	SEQ ID	NO: 4	:								
169	(i) SEQU												
170			: 136 ai			s							
171			amino a			_							
172		STRAND											
173			GY: line	ear									
179	(xi) SEQU	ENCE DE	SCRIPTIO	ON: S	eio m	. אט	٠ ٨٠						
181	Glu Asp	Glu Ser	Thr Va	Len	Val	Aen	λen	Tue	Cvr	C1.	Cura	14. 1	
182	1		5	. 100	142	пэр	10	БУЗ	Cys	OLII	Cys		Arg
1.84	Ile Thr	Ser Ara		> Ara	Aen	Dro		Tan	Dane	C	<b>a</b> 1	15	- 1
185		20		9	21 [5	25	vab	иоп	PIO	Set		Asp	11.e
187	Val Glu		Tle Arc	Tle	Tla		Dro	rou	Aan	rn L	30	a1	
1.88		35		,	40	¥ C4 1.	1.1.0	neu	ASII		A.r.g	GLU	Asn
190	Ile Ser	Asp Pro	Thr Ser	Pro		λκα	Thr	Clu	Dwo	45	(0		
191	50		001	55	DCu	n.i. g	111.1.	G.L.u	60	пÀВ	TYL	ASI	reu
193	Ala Asn	Leu Cvs	Lvs Lvs		Aen	Dro	nih r	C1.,	1130	<i>α</i> 1	·		
194	65		70	, 0,5	nsp.	110		75	116	GAU	ren	Asp	
196	Gln Val I	Phe Thr		Gln	Sor	λen	Tlo	CVC	Dro	3	3		80
197			85	OZII	CL		90	Cys	P1.0	asp	ASP		TYT
199	Ser Glu	Thr Cvs		mv.r	Aca			f +	C		m l	95	
200		100	171 1111	171	nap	105	ASII .	гàг	Cys	Tyr		THY	Leu
202	Val Pro		His Ara	Glv	Va 1	The	A secret	Mot	370.1	T	110	ml	
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205	Thr Pro A		Cvs Tvr	Pro						123			
206	130		010 111	135	нэр								
208 (2)	INFORMATIO	N FOR S	EO TD N										
210	(i) SEQUE	NCE CHA	RACTERT	STICS									
211			119 am										
212			mino ac		0.2(2.5								
21.3		STRANDE		3. 0									
214			Y: line	ar									
220	(xi) SEQUE				O TD	NO.	5.						
222	Glu Gln G	lu Tvr	Tle Leu	Δla	Q LD Δen i	NO. Non 1	J: Tugʻ	· ·	Liva	0	171	·	- 1
223	1	7	5	71.1.C	asii i	1 1167	Lys ( LO	- y S	Lys	Cys			Tire
225	Ser Ser A	ra Phe	val pro	Sar	The C	23 0 7	lva E	)·no	on	a1	01	15	
226	•	20		002		25	rra r	10	GTJ .			ire.	Leu
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229	3	5			40			,cı		arg. 45	met.	naa .	тте
231	Ser Asp P	ro Tyr :	Ser Pro			Thr G	ilo D	ro .	/al (	TUY :	Ace :	[ A ]	Two
232	50			55	9	ی مید	and I		var. :	T X T	1311	neu ,	rrp

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Input Set : A:\401c1.app
Output Set: N:\CRF3\02062001\1005318C.raw

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	234 235		6.5	)					70				. Glm	75					80	
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	238							85					90					95	_	
	240		Ту	r Th	ir Ti	ır G	Lu	Val	Asn	Phe	Lys		Lys	Val	Pro	Leu	Thr	Pro	Asp	
	241. 243		Co	- Cu	a m-		.00	D1.	41			1.05					110			
	244		56	er cy	s Ty		Tu	тyr	Ser	G.I u										
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	259		(xi	) SE	QUEN	CE	DES	CRI	PTIO	N: S	EQ I	D NO	: 6:							
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	262		1					5					10					1.5	-	
	264		GI	u As	b br	O A	sn (	GLu	Asp	lle	Val	Glu	Arg	Туr	He	Arg	Ile	Asn	Val	
	265					2						25					30			
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	274		65	. 01	u ma	ЬО	т.у	vaı	70	1111	HIA	THE	GTII	75	Asn	TTE	Cys	Tyr		
	276			p G1.	n Gl	v V	al I	Pro		Ser	Cvs	Ara	Asp	7J Wyr	Cue	Bro	C1.0	Tou	80	
	277						8	35		., ., _	0/1.	**** 9	90	1 y 1.	Cys	FIU	GLU	95	ASP	
	279		Arc	ÿ Ası	n Ly	s C	ys :	ryr	Thr	Val	Leu	Val	Pro	Pro	Glv	Tvr	Thr	Glv	Gln	
	280					1	0.0	-				105			,7	- 1 -	110	O.C.J	01.4	
	282		Thi	r Ly:	s Me	t. Va	al (	31.n	Asn	Ala	Leu	Thr	Pro	Asp	Ala	Cys	Tyr	Pro	Asp	
	283				1.1	5					120			•		125	•			
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	298								41	4										
	301.		(xi.)								O II	NO:	7 .							
;	303	GАT	CAG	GAA	GAT	GAA	CG	TA	TT G	TT C	TG	тт с	AC A	AC A	AG T	GC A	AG T	GT		48
:	304	Asp	Gln	Glu	Asp	Glu	Ar	g I	le v	al I	eu \	al A	sp A	sn L	vs C	vs L	vs C	vs		40
	305	3.				5						10					15			
	307 (	GCT	CGT	ATT	АСТ	TCI	' AG	A A	TC A	TC C	GT A	GC T	'CA G	AG G	AC C	CA A	AT G	AA		96
-	308	Ala	Arg	Ile	Thr	ser	Ar	g I	le I	le A	rg S	er s	er G	lu A	sp P	ro A	sn G	lu		
3	309				20						25					30				
3	11.	JA'l'	ATA	GTC	GAA	CGT	AA	C A	TC C	GT A	TC A	TC G	TC C	CA C	TG A	АТ А	AC C	GG		1.44
3	2.12 1	48b	Ile	val	GIU	arg	AS	n I.	re y	rg I	Te I	le V	al P	ro L	eu A	sn A	sn A	rg		

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/005,318C

DATE: 02/06/2001 TIME: 15:57:09

Input Set : A:\401c1.app
Output Set: N:\CRF3\02062001\1005318C.raw

313			35					40					45				
	GAG	дат		TCA	CAT	ССТ	ACA	AGT	ccc	ሞሞሮ	ccc	ΔΟΔ		יייייר	CIPA	መአር	192
								Ser									1.52
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	CAC		TCA	GAT	CTG	тст		AAG	יניסיני	GAT	CCA		GAG	CTA	GAG	CTG	240
								Lys									240
321	65		0 4.51	of-	3500	70	13] 5	2.7.5	010	n.	75	1113.	OLG	V (L 1.	CITU	80	
		AAT	CAG	ATA	GTC		GCG	ACT	CAA	AGC		Δηνη	PGC	יויעט	CAC		288
								Thr									200
325					85				0	90	,		910	map	95	11313	
327	AGC	GCT	ACA	GAA	ACC	TGC	AGC	ACC	TAC		AGC	AAC	AAA	TGC		ACG	336
328	ser	Ala	Thr	Glu	Thr	Cvs	Ser	Thr	Tvr	Asp	Arg	Asn	Lvs	CVS	Tivr	Thr	330
329				1.00		. 1			105				, .	110	1. 1		
331	GCC	GTG	GTT	CCG	CTC	GTG	TAT	GGT		GAG	ACA	ΑΑΛ	ATG		CAA	АСТ	384
332	Ala	Val	Val	Pro	Leu	Val	Tyr	Gly	Glv	Glu	Thr	Lvs	Met.	Val	Glu	Thr	30.
333			115				,	1.20				-2-	1.25		0 0		
335	GCC	CTT	ACG	CCC	GAT	GCA	TGC	TAT	CCG	GAC	TGAZ	ATTC					421
								Tyr									
337		130			•		135	٠		•							
340	(2)	INFO	DRMA'	rion	FOR	SEQ	ID 1	NO: 8	3 :								
342								ISTIC									
343			( /	A) LI	ENGTE	1: 2.	15 ba	ase p	airs	3							
344			(1	3) TY	PE:	nucl	leic	acio	i								
345			((	C) Si	PRANI	DEDNI	ESS:	sing	jle								
346			1)	) TO	POLC	GY:	line	ear									
350		(ix)	) FE	ATURI	ß :												
35.1																	
331			( 2	1) NA	ME/F	EY:	CDS										
352				1) NA 3) LO				213									
		(xi)	( I	3) LC	САТ	ON:	12	213 ON: 5	SEQ 1	D NO	): 8:						
352 355 357		CAG	(E SEC	B) LO QUENO TGC	CATI CE DE AAG	ON: ESCRI TGT	12 PTIC GCT	ON: S CGT	ATT	ACT	TCT	AGA					48
352 355 357 358	Asp	CAG	(E SEC	B) LO QUENO TGC	CATI CE DE AAG Lys	ON: ESCRI TGT	12 PTIC GCT	ON: 5	ATT	ACT	TCT	AGA					48
352 355 357 358 359	Asp 1	CAG Gln	(H SE( AAG Lys	OUENC TGC Cys	CATI CE DE AAG Lys 5	ON: ESCRI TGT Cys	12 PTIC GCT Ala	ON: S CGT Arg	ATT Ile	ACT Thr 10	TCT Ser	AGA Arg	Ile	Ile	Arg 15	Ser	48
352 355 357 358 359 361	Asp 1 TCA	CAG Gln GAG	(E) SE( AAG Lys GAC	DUENC TGC Cys	CATI CE DE AAG Lys 5 AAT	ON: ESCRI TGT Cys GAA	12 PTIC GCT Ala GAT	ON: S CGT Arg ATA	ATT Ile GTC	ACT Thr 10 GAA	TCT Ser CGT	AGA Arg AAC	Ile ATC	Ile CGT	Arg 15 ATC	Ser ATC	48 96
352 355 357 358 359 361 362	Asp 1 TCA	CAG Gln GAG	(E) SE( AAG Lys GAC	OUENC TGC Cys CCA Pro	CATI CE DE AAG Lys 5 AAT	ON: ESCRI TGT Cys GAA	12 PTIC GCT Ala GAT	ON: S CGT Arg	ATT Ile GTC Val	ACT Thr 10 GAA	TCT Ser CGT	AGA Arg AAC	Ile ATC	Ile CGT Arg	Arg 15 ATC	Ser ATC	
352 355 357 358 359 361 362 363	Asp 1 TCA Ser	CAG Gln GAG Glu	(H AAG Lys GAC Asp	DUENC TGC Cys CCA Pro 20	CATT CE DE AAG Lys 5 AAT ASD	CON: ESCRI TGT Cys GAA Glu	12 IPTIC GCT Ala GAT ASP	ON: S CGT Arg ATA Ile	ATT Ile GTC Val 25	ACT Thr 10 GAA Glu	TCT Ser CGT Arg	AGA Arg AAC Asn	Ile ATC Ile	Ile CGT Arg 30	Arg 15 ATC Ile	Ser ATC Ile	96
352 355 357 358 359 361 362 363 365	Asp 1 TCA Ser GTC	CAG Gln GAG Glu CCA	(HAAG Lys GAC Asp CTG	DUENC TGC Cys CCA Pro 20 AAT	OCATI DE DE AAG Lys 5 AAT ASD	CON: ESCRI TGT CYS GAA Glu CGG	12 CPTIC GCT Ala GAT Asp	ON: S CGT Arg ATA ILE AAT	ATT Ile GTC Val 25 ATC	ACT Thr 10 GAA Glu TCA	TCT Ser CGT Arg	AGA Arg AAC Asn	Tle ATC Ile ACA	CGT Arg 30 AGT	Arg 15 ATC Ile CCG	Ser ATC Ile	
352 355 357 358 359 361 362 363 365 366	Asp 1 TCA Ser GTC	CAG Gln GAG Glu CCA	(H) SEG AAG Lys GAC Asp CTG Leu	DUENC TGC Cys CCA Pro 20 AAT	OCATI DE DE AAG Lys 5 AAT ASD	CON: ESCRI TGT CYS GAA Glu CGG	12 CPTIC GCT Ala GAT Asp	ON: S CGT Arg ATA Ile AAT Asn	ATT Ile GTC Val 25 ATC	ACT Thr 10 GAA Glu TCA	TCT Ser CGT Arg	AGA Arg AAC Asn	ATC Ile ACA Thr	CGT Arg 30 AGT	Arg 15 ATC Ile CCG	Ser ATC Ile	96
352 355 357 358 359 361 362 363 365 366 367	Asp 1. TCA Ser GTC Val.	CAG Gln GAG Glu CCA Pro	(H) SEC AAG Lys GAC Asp CTG Leu 35	DUENC TGC Cys CCA Pro 20 AAT Asn	DCATE DE DE AAG Lys 5 AAT AST AAC AST	ON: ESCRI TGT Cys GAA Glu CGG Arg	12 IPTIC GCT Ala GAT ASP GAG Glu	ON: S CGT Arg ATA Ile AAT Asn 40	ATT Ile GTC Val 25 ATC Ile	ACT Thr 10 GAA Glu TCA Ser	TCT Ser CGT Arg GAT Asp	AGA Arg AAC Asn CCT Pro	ATC Ile ACA Thr 45	CGT Arg 30 AGT Ser	Arg 15 ATC Ile CCG Pro	Ser ATC Ile TTG Leu	96 144
352 355 357 358 359 361 362 363 365 365 367 369	Asp 1 TCA Ser GTC Val.	CAG Gln GAG Glu CCA Pro	GAC Asp CTG Leu 35 CGC	DUENC TGC Cys CCA Pro 20 AAT Asn	DCATE DE DE AAG Lys 5 AAT Asn AAC Asn	ON: ESCRI TGT Cys GAA Glu CGG Arg	12 PTIC GCT Ala GAT Asp GAG Glu	ON: S CGT Arg ATA Ile AAT Asn 40 CTG	ATT Ile GTC Val 25 ATC Ile TCA	ACT Thr 10 GAA GIU TCA Ser GAT	TCT Ser CGT Arg GAT Asp	AGA Arg AAC Asn CCT Pro	ATC Ile ACA Thr 45 AAG	CGT Arg 30 AGT Ser	Arg 15 ATC Ile CCG Pro	Ser ATC Ile TTG Leu GAG	96
352 355 357 358 359 361 362 363 365 366 367 369 370	Asp 1 TCA Ser GTC Val.	CAG Gln GAG Glu CCA Pro ACA Thr	GAC Asp CTG Leu 35 CGC	DUENC TGC Cys CCA Pro 20 AAT Asn	DCATE DE DE AAG Lys 5 AAT Asn AAC Asn	ON: ESCRI TGT Cys GAA Glu CGG Arg	12 PTIC GCT Ala GAT ASP GAG Glu CAC	ON: S CGT Arg ATA Ile AAT Asn 40	ATT Ile GTC Val 25 ATC Ile TCA	ACT Thr 10 GAA GIU TCA Ser GAT	TCT Ser CGT Arg GAT Asp	AGA Arg AAC Asn CCT Pro TGT Cys	ATC Ile ACA Thr 45 AAG	CGT Arg 30 AGT Ser	Arg 15 ATC Ile CCG Pro	Ser ATC Ile TTG Leu GAG	96 144
352 355 357 358 359 361 362 363 365 366 367 369 370 371	Asp 1 TCA Ser GTC Val CGC Arg	CAG Gln GAG Glu CCA Pro ACA Thr 50	GAC ASP CTG Leu 35 CGC Arg	B) LC QUENC TGC Cys CCA Pro 20 AAT Asn TTC	DE DE AAG Lys 5 AAT ASN AAC ASN GTA Val	CON: ESCRITGT Cys GAA Glu CGG Arg TAC Tyr	PTIC GCT Ala GAT Asp GAG Glu CAC His	ON: S CGT Arg ATA Ile AAT Asn 40 CTG Leu	ATT Ile GTC Val 25 ATC Ile TCA	ACT Thr 10 GAA GIU TCA Ser GAT	TCT Ser CGT Arg GAT Asp	AGA Arg AAC Asn CCT Pro	ATC Ile ACA Thr 45 AAG	CGT Arg 30 AGT Ser	Arg 15 ATC Ile CCG Pro	Ser ATC Ile TTG Leu GAG	96 144 192
352 355 357 358 359 361 362 363 365 366 367 369 371 373	Asp 1 TCA Ser GTC Val. CGC Arg	CAG Gln GAG Glu CCA Pro ACA Thr 50 AGC	(H) SEC AAG Lys GAC Asp CTG Leu 35 CGC Arg	B) LC QUENC TGC Cys CCA Pro 20 AAT Asn TTC Phe	DE DE AAG LYS SAAT ASN AAC ASN GTA Val	CON: ESCRITGT Cys GAA Glu CGG Arg TAC Tyr	TPTIC GCT Ala GAT Asp GAG Glu CAC His 55	ON: S CGT Arg ATA Ile AAT Asn 40 CTG Leu	ATT Ile GTC Val 25 ATC Ile TCA	ACT Thr 10 GAA GIU TCA Ser GAT	TCT Ser CGT Arg GAT Asp	AGA Arg AAC Asn CCT Pro TGT Cys	ATC Ile ACA Thr 45 AAG	CGT Arg 30 AGT Ser	Arg 15 ATC Ile CCG Pro	Ser ATC Ile TTG Leu GAG	96 144
352 355 357 358 359 361 362 365 366 367 369 370 371 373 374	Asp 1 TCA Ser GTC Val. CGC Arg GAC Asp	CAG Gln GAG Glu CCA Pro ACA Thr 50 AGC	(H) SEC AAG Lys GAC Asp CTG Leu 35 CGC Arg	B) LC QUENC TGC Cys CCA Pro 20 AAT Asn TTC	DE DE AAG LYS SAAT ASN AAC ASN GTA Val	CON: ESCRITGT Cys GAA Glu CGG Arg TAC Tyr ACC Thr	TPTIC GCT Ala GAT Asp GAG Glu CAC His 55	ON: S CGT Arg ATA Ile AAT Asn 40 CTG Leu	ATT Ile GTC Val 25 ATC Ile TCA	ACT Thr 10 GAA GIU TCA Ser GAT	TCT Ser CGT Arg GAT Asp	AGA Arg AAC Asn CCT Pro TGT Cys	ATC Ile ACA Thr 45 AAG	CGT Arg 30 AGT Ser	Arg 15 ATC Ile CCG Pro	Ser ATC Ile TTG Leu GAG	96 144 192
352 355 357 358 359 361 362 363 365 366 367 369 370 371 373 374 375	Asp 1 TCA Ser GTC Val CGC Arg GAC Asp 65	CAG Gln GAG Glu CCA Pro ACA Thr 50 AGC Ser	GAC Asp CTG Leu 35 CGC Arg GCT Ala	B) LO QUENC TGC Cys CCA Pro 20 AAT Asn TTC Phe ACA Thr	DCATE DE DE AAG Lys 5 AAT ASD AAC ASD GTA Val GAA Glu	CON: ESCRITGT Cys GAA Glu CGG Arg TAC Tyr ACC Thr 70	CAC His TGC TGC TGC TGC	ON: S CGT Arg ATA Ile AAT Asn 40 CTG Leu	ATT Ile GTC Val 25 ATC Ile TCA Ser	ACT Thr 10 GAA GIU TCA Ser GAT	TCT Ser CGT Arg GAT Asp	AGA Arg AAC Asn CCT Pro TGT Cys	ATC Ile ACA Thr 45 AAG	CGT Arg 30 AGT Ser	Arg 15 ATC Ile CCG Pro	Ser ATC Ile TTG Leu GAG	96 144 192
352 355 357 358 359 361 362 363 365 366 367 369 371 373 374 375 378	Asp 1 TCA Ser GTC Val CGC Arg GAC Asp 65	CAG Gln GAG Glu CCA Pro ACA Thr 50 AGC Ser	(H) SEC AAG Lys GAC Asp CTG Leu 35 CGC Arg GCT Ala	3) LC QUENC TGC Cys CCA Pro 20 AAT Asn TTC Phe ACA Thr	DCATE DE DE AAG Lys 5 AAT ASD AAC ASD GTA Val GAA Glu FOR	CON: ESCRITGT Cys GAA Glu CGG Arg TAC Tyr ACC Thr 70 SEQ	12 TPTIC GCT Ala GAT Asp GAG Glu CAC His 55 TGC Cys	ON: S CGT Arg ATA Ile AAT ASN 40 CTG Leu TG	ATT Ile GTC Val 25 ATC Ile TCA Ser	ACT Thr 10 GAA GIU TCA Ser GAT	TCT Ser CGT Arg GAT Asp	AGA Arg AAC Asn CCT Pro TGT Cys	ATC Ile ACA Thr 45 AAG	CGT Arg 30 AGT Ser	Arg 15 ATC Ile CCG Pro	Ser ATC Ile TTG Leu GAG	96 144 192
352 355 357 358 359 361 362 363 365 366 367 370 371 373 374 375 378	Asp 1 TCA Ser GTC Val CGC Arg GAC Asp 65	CAG Gln GAG Glu CCA Pro ACA Thr 50 AGC Ser	(T) SE( AAG Lys GAC Asp CTG Leu 35 CGC Arg GCT Ala	3) LCQUENC TGC Cys CCA Pro 20 AAT Asn TTC Phe ACA Thr	CATH AAG Lys 5 AAT ASH AAC ASH GTA Val GAA Glu FOR E CH	CON: CSCRI TGT Cys GAA Glu CGG Arg TAC Tyr ACC Thr 70 SEQ ARAC	12 PPTIC GCT Ala GAT ASP GAG Glu CAC His 55 TGC Cys	ON: S CGT Arg ATA Ile AAT ASN 40 CTG Leu TG	ATT Ile GTC Val 25 ATC Ile TCA Ser	ACT Thr 10 GAA GIU TCA Ser GAT ASP	TCT Ser CGT Arg GAT Asp	AGA Arg AAC Asn CCT Pro TGT Cys	ATC Ile ACA Thr 45 AAG	CGT Arg 30 AGT Ser	Arg 15 ATC Ile CCG Pro	Ser ATC Ile TTG Leu GAG	96 144 192
352 355 357 358 359 361 362 363 365 366 367 370 371 373 374 375 380 381	Asp 1 TCA Ser GTC Val CGC Arg GAC Asp 65	CAG Gln GAG Glu CCA Pro ACA Thr 50 AGC Ser	(H) SECA AAG Lys GAC Asp CTG Leu 35 CGC Arg GCT Ala	3) LC QUENC TGC CYS CCA Pro 20 AAT ASn TTC Phe ACA Thr UENC	OCATH DE DE AAG LYS 5 AAT ASN AAC ASN GTA Val GAA Glu FOR E CH	CON: ESCRITGT Cys GAA Glu CGG Arg TAC Tyr ACC Thr 70 SEQ ARACC: 14	12 GCT Ala GAT Asp GAG Glu CAC His 55 TGC Cys	ON: SCOT Arg ATA Ile AAT ASN 40 CTG Leu TG	ATT Ile GTC Val 25 ATC Ile TCA Ser : S: airs	ACT Thr 10 GAA GIU TCA Ser GAT ASP	TCT Ser CGT Arg GAT Asp	AGA Arg AAC Asn CCT Pro TGT Cys	ATC Ile ACA Thr 45 AAG	CGT Arg 30 AGT Ser	Arg 15 ATC Ile CCG Pro	Ser ATC Ile TTG Leu GAG	96 144 192
352 355 357 358 359 361 362 363 365 366 367 370 371 373 374 375 378	Asp 1 TCA Ser GTC Val CGC Arg GAC Asp 65	CAG Gln GAG Glu CCA Pro ACA Thr 50 AGC Ser	(H) SEQ AAG Lys GAC Asp CTG Leu 35 CGC Arg GCT Ala SEQ (A GCT A GC	3) LCQUENCE TGC CYS CCA Pro 20 AAT ASn TTC Phe ACA Thr CUENCE CYS TYON LEECT TYS	OCATI DE DE AAG LYS 5 AAT ASN AAC ASN GTA Val GAA Glu FOR E CH NNGTH PE:	CON: CSCRI TGT Cys GAA Glu CGG Arg TAC Tyr ACC Thr 70 SEQ ARACC: 14	12 GCT Ala GAT ASP GAG GLU CAC His 55 TGC CYS ID N TERIO 0 ba	ON: S CGT Arg ATA Ile AAT ASN 40 CTG Leu TG	ATT Ile GTC Val 25 ATC Ile TCA Ser :	ACT Thr 10 GAA GIU TCA Ser GAT ASP	TCT Ser CGT Arg GAT Asp	AGA Arg AAC Asn CCT Pro TGT Cys	ATC Ile ACA Thr 45 AAG	CGT Arg 30 AGT Ser	Arg 15 ATC Ile CCG Pro	Ser ATC Ile TTG Leu GAG	96 144 192

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/005,318C

DATE: 02/06/2001 TIME: 15:57:10

Input Set : A:\401c1.app

Output Set: N:\CRF3\02062001\1005318C.raw

L:6 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]
L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:] L:20 M:220 C: Reyword misspelled or invalid format, [(B)]
L:228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:237 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:2470 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:118
L:2473 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:118
L:2624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:123
L:2630 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:123
L:2633 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:123